

Genome version 5.1.6
Copyright (c) 1995 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 10:46:44 / Search time 30.8071 seconds

(without alignment)
1457.493 Million cell updates/sec

Title: US-10-067-385-8_copy_600_773

Sequence: 1 KLVGPPNRRITVYKPSILMK.....ATVLDNNISSTNPNK 174

Scoring table: BLOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 835525 seqs, 238055604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 5

Maximum DB seq length: 500000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Filtering filter 49 summaries

Database: SPREDDBL_23:*

1: sp.archaea:*

2: sp.bacteria:*

3: sp.fungi:*

4: sp.human:*

5: sp.invertebrate:*

6: sp.mammal:*

7: sp.mollusc:*

8: sp.organelle:*

9: sp.phage:*

10: sp.plant:*

11: sp.reptile:*

12: sp.virus:*

13: sp.vertebrate:*

14: sp.unclassified:*

15: sp.virus:*

16: sp.bacteriophage:*

17: sp.archaeo:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SDNNMAIS

Result	Query	Score	Match	Length	DB ID	Description
1	897	100.0	2119	2	Q9ATY5	Q9ATY5 streptococ
2	897	100.0	2140	16	Q9ATY6	Q9ATY6 streptococ
3	894	99.7	2144	16	Q9ATY7	Q9ATY7 streptococ
4	894	99.7	2144	16	Q9ATY8	Q9ATY8 streptococ
5	113	13.3	375	16	Q9ATY9	Q9ATY9 streptococ
6	114.5	12.8	1038	13	Q9ATY8	Q9ATY8 streptococ
7	114	12.7	609	5	Q9ATY8	Q9ATY8 streptococ
8	114.5	12.8	1038	13	Q9ATY8	Q9ATY8 streptococ
9	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
10	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
11	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
12	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
13	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
14	110.5	12.4	379	5	Q9ATY5	Q9ATY5 streptococ
15	110.5	12.3	380	5	Q9ATY5	Q9ATY5 streptococ
16	110	12.3	380	5	Q9ATY5	Q9ATY5 streptococ

Result	Query	Score	Match	Length	DB ID	Description
1	897	100.0	2119	2	Q9ATY5	Q9ATY5 streptococ
2	897	100.0	2140	16	Q9ATY6	Q9ATY6 streptococ
3	894	99.7	2144	16	Q9ATY7	Q9ATY7 streptococ
4	894	99.7	2144	16	Q9ATY8	Q9ATY8 streptococ
5	113	13.3	375	16	Q9ATY9	Q9ATY9 streptococ
6	114.5	12.8	1038	13	Q9ATY8	Q9ATY8 streptococ
7	114	12.7	609	5	Q9ATY8	Q9ATY8 streptococ
8	114.5	12.8	1038	13	Q9ATY8	Q9ATY8 streptococ
9	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
10	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
11	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
12	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
13	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
14	110.5	12.4	379	5	Q9ATY5	Q9ATY5 streptococ
15	110.5	12.3	380	5	Q9ATY5	Q9ATY5 streptococ
16	110	12.3	380	5	Q9ATY5	Q9ATY5 streptococ

ALIGNMENTS

Result	Query	Score	Match	Length	DB ID	Description
1	897	100.0	2119	2	Q9ATY5	Q9ATY5 streptococ
2	897	100.0	2140	16	Q9ATY6	Q9ATY6 streptococ
3	894	99.7	2144	16	Q9ATY7	Q9ATY7 streptococ
4	894	99.7	2144	16	Q9ATY8	Q9ATY8 streptococ
5	113	13.3	375	16	Q9ATY9	Q9ATY9 streptococ
6	114.5	12.8	1038	13	Q9ATY8	Q9ATY8 streptococ
7	114	12.7	609	5	Q9ATY8	Q9ATY8 streptococ
8	114.5	12.8	1038	13	Q9ATY8	Q9ATY8 streptococ
9	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
10	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
11	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
12	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
13	112.5	12.5	354	5	Q9ATY5	Q9ATY5 streptococ
14	110.5	12.4	379	5	Q9ATY5	Q9ATY5 streptococ
15	110.5	12.3	380	5	Q9ATY5	Q9ATY5 streptococ
16	110	12.3	380	5	Q9ATY5	Q9ATY5 streptococ

[illegible]

McFadden G.J., Cummings L.M., Subramanian G.M., Mungall C.J., Fraser C.W., Barrett B., Hottel S.L., Newbold C., Davis R.N., RT "Genome sequence of the human malaria parasite *Plasmodium falciparum*." Science 286:1551-1571 (1999)
 RT "Genome sequence of the human malaria parasite *Plasmodium falciparum*." EMBL:1801486-1801524.11
 DB Initiation factor.
 SO SEQUENCE 1377 AA; 166059 MW; 587CF2E3F2C8F89 CRC64;

Query Match 11.38; Score 101.5; DB 5; Length 1377;
 Seqc Local Similarity 22.38; Pred. no. 61; Matches 9;
 Matches 43; Conservative 37; Mismatches 62; Indels 51; Gaps 9;

QY 13 VKEPIILNMGSGSELEHRYTYTTONER--WSTIVSGEPIILPVGEELENGOF--68
 DB 619 IKSLINWYNDLQGLIYHMETIATISNRYMWTETLTREEP--ATDSNKNINMT 675
 QY 69 ----DQETSGEGEDMDQVYINLSQPTIYVPTKLEF-----KERNYTPNKK 117
 DB 676 ATLENTISNVEPERF-----IEMELAKTYEKIDBEHKQLLSRRNNKKRKLK 728
 QY 118 KENQYPMHSGLR-----SSNKKRQOR-----HNSGNSSTQYVAT 156
 DB 729 HQ--KELHQQQLKIMHKKLSEKVLKKEKKERLAKNKKLAKIKERHKKKLEADQWLR 786
 QY 157 VLNNYISSTMT 169
 DB 787 I--KQLCSPTPT 796

Search completed: February 10, 2004, 10:57:11
 Job time : 32.8071 secs

GenDoc version 5.1.6
Copyright (c) 1993-2004 CompuGen Ltd.

OW protein - protein search, using nw model
Run on: February 10, 2004, 10:48:45, Search time 12,5638 Seconds
(without alignments)
131,870 Million cell updates/sec

Title: US-10-067-385-8_COPY_600_773
Perfect score: 897
Sequence: 1 XIYVQPNANTYKTEPLINK.....ATVADONNSSTNNRK 174
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616682 residues
Total number of hits satisfying chosen parameters: 283308

Maximum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 10
Maximum Match 100
Matching filter to eliminate

Database: 1: pr1;
2: pr2;
3: pr3;
4: pr4;

Pred. No. is the number of reviews predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	897	100.0	2140	P95074	serine proteinase,
2	894	99.7	2144	A97942	classenrin - chikc
3	114.5	12.8	1038	J05947	classenrin - chikc
4	109	12.2	665	871609	hypothetical prote
5	104	11.6	540	D86432	hypothetical prote
6	103.5	11.5	325	T19233	hypothetical prote
7	102.5	11.4	285	T40570	hypothetical prote
8	101.5	11.3	312	G81139	probable membrane
9	101.5	11.3	535	T73189	hypothetical prote
10	101.5	11.3	208	S67250	hypothetical prote
11	101.5	11.3	208	S67250	hypothetical prote
12	100	11.1	1875	S38133	myosin-like protei
13	100	11.1	211	T75911	hypothetical prote
14	99	11.0	211	T75911	hypothetical prote
15	99	11.0	211	T75911	hypothetical prote
16	97.5	10.9	1345	S66837	hypothetical prote
17	97.5	10.9	1345	S66837	hypothetical prote
18	97.5	10.9	1345	S66837	hypothetical prote
19	97	10.8	644	T74185	hypothetical prote
20	96.5	10.8	867	T73135	hypothetical prote
21	96.5	10.8	867	T73135	hypothetical prote
22	96.5	10.8	867	T73135	hypothetical prote
23	96.5	10.8	867	T73135	hypothetical prote
24	96	10.7	1393	C74057	hypothetical prote
25	96	10.7	1393	C74057	hypothetical prote
26	96	10.7	2500	G71609	hypothetical prote
27	95.5	10.6	3742	T17471	hypothetical prote
28	95	10.6	348	T17471	hypothetical prote
29	95	10.6	1202	I505362	probable DNA direct

30	94.5	10.5	277	D70214	surface lipoprotei
31	94.5	10.5	670	T28391	ORF MS230 hypoch
32	94	10.5	210	T28771	hypothetical prote
33	94	10.5	553	T15094	hypothetical prote
34	93.5	10.4	456	T10345	hypothetical prote
35	93.5	10.4	456	T10345	hypothetical prote
36	93.5	10.4	645	S89883	conserved hypoch
37	93.5	10.4	645	S89883	conserved hypoch
38	93	10.4	649	S24488	ORF MS230 hypoch
39	93	10.4	649	S24488	ORF MS230 hypoch
40	92.5	10.3	443	S66040	hypothetical prote
41	92.5	10.3	443	S66040	hypothetical prote
42	92.5	10.3	571	T86469	hypothetical prote
43	92.5	10.3	1482	T13009	hypothetical prote
44	92.5	10.3	1997	T71607	hypothetical prote
45	92	10.3	688	A47705	trialcylglycerol 11

ALIGNMENTS

FIGURE 1

serine proteinase, subtilase family [imported] - Streptococcus pneumoniae (strain TIGR P95074)

C.Species: Streptococcus pneumoniae

C.Date: 03-Aug-2001 Sequence_Revision: 03-Aug-2001 Hecot_change: 03-Aug-2001

C.Project: 03-Aug-2001 Sequence_Revision: 03-Aug-2001 Hecot_change: 03-Aug-2001

C.Author: J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

on, J.D. Nelson, K.R. Paulsen, I.T. Eisen, J.A. Bead, T.D. Peterson, S.J. He

C Date: 10-Sep-1999 #sequence_rev100 Sep-1999 #cont_change 28-Jul-2000
 C accession: T14188
 R: Jensen, M.; Lemaire, N.; Quail, M.; Harris, B.; Rajadurai, M.A.; Barrall, B.G.; Banerjee, submitted to the Protein Sequence Database, August 1999
 A reference: T14188
 A molecule type: DNA
 A residues: 1-988

 A description: BMDA110819
 A experimental source: Cultivar Columbia; BAC clone T7805
 C identifier:
 A gene: AT5G7805.30
 A map position: 31, 201/3, 416/3, 438/3, 460/3, 482/3, 504/3, 519/3, 534/3, 559/3, 579/3;
 C superfamily: Arabidopsis thaliana hypothetical protein T2C14.40

Query Match 10.8% Score 97; DB 2; Length 988;
 Best local similarity 25.0%; Pred. No. 10;
 Matches 45; Conservative 31; Mismatches 67; Indels 22; Gaps 5

39 KXGKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 93
 Db MGRGKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 441
 383 MGRGKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 441
 94 KXGKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 142
 Db MGRGKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 501
 442 VFNQDVSQDQSPKAPKANNVAPKATPDSIKQDVAQVADIKSLQSLP 501
 143 HSKGKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 174
 502 HVL---GADVTVDSQDQSPKAPKANNVAPKATPDSIKQDVAQVADIKSLQSLP 532

RESULT 21
 T05412
 hypothetical protein PPD6.270 - Arabidopsis thaliana
 C Species: Arabidopsis thaliana (mouse-ear cress)
 C accession: T05412
 C Date: 23-Apr-1999 #sequence_rev100 Apr-1999 #cont_change 23-Jul-1999
 R: Jensen, M.; Medler, H.; Medler, B.; Neubauer, R.; Hobelet, J.; Mewes, H.W.; Meyer, K.F. submitted to the Protein Sequence Database, February 1999
 A reference number: T15419
 A molecule type: DNA
 A residues: 1-456

 A description: BMDA103394
 A experimental source: Cultivar Columbia; BAC clone PPD6
 C identifier:
 A map position: 4
 A introns: 110/3, 247/3, 282/3, 304/3, 361/3, 390/3, 418/3
 A notes: PPD6.270

Query Match 10.8% Score 96.5; DB 2; Length 456;
 Best local similarity 25.0%; Pred. No. 10;
 Matches 40; Conservative 29; Mismatches 61; Indels 31; Gaps 8

20 KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 78
 Db KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 296
 245 KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 136
 79 KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 136
 Db KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 345
 297 KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 345
 137 QVREHNSQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 174
 346 ALQVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 378

RESULT 22
 T21315
 hypothetical protein Y5C12B.3a - Caenorhabditis elegans
 C Species: Caenorhabditis elegans
 C accession: T21315
 C Date: 15-Oct-1999 #sequence_rev100 Oct-1999 #cont_change 15-Oct-1999
 R: Jensen, M.; Lemaire, N.; Quail, M.; Harris, B.; Rajadurai, M.A.; Barrall, B.G.; Banerjee, submitted to the Protein Sequence Database, August 1999
 A reference: T21315
 A molecule type: DNA
 A residues: 1-988

 A description: BMDA110819
 A experimental source: Cultivar Columbia; BAC clone T7805
 C identifier:
 A gene: AT5G7805.30
 A map position: 31, 201/3, 416/3, 438/3, 460/3, 482/3, 504/3, 519/3, 534/3, 559/3, 579/3;
 C superfamily: Arabidopsis thaliana hypothetical protein T2C14.40

C Date: 15-Oct-1999 #sequence_rev100 Oct-1999 #cont_change 15-Oct-1999
 C accession: T21315
 R: Jensen, M.; Lemaire, N.; Quail, M.; Harris, B.; Rajadurai, M.A.; Barrall, B.G.; Banerjee, submitted to the Protein Sequence Database, August 1999
 A reference: T21315
 A molecule type: DNA
 A residues: 1-988

 A description: BMDA110819
 A experimental source: Cultivar Columbia; BAC clone T7805
 C identifier:
 A gene: AT5G7805.30
 A map position: 31, 201/3, 416/3, 438/3, 460/3, 482/3, 504/3, 519/3, 534/3, 559/3, 579/3;
 C superfamily: Arabidopsis thaliana hypothetical protein T2C14.40

Query Match 10.8% Score 96.5; DB 2; Length 867;
 Best local similarity 25.0%; Pred. No. 21;
 Matches 45; Conservative 31; Mismatches 63; Indels 39; Gaps 8

9 KATVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 52
 Db KATVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 695
 63 K---KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 114
 Db KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 174
 696 KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 174
 748 KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 805

RESULT 23
 T21315
 hypothetical protein Y5C12B.3b - Caenorhabditis elegans
 C Species: Caenorhabditis elegans
 C accession: T21315
 C Date: 15-Oct-1999 #sequence_rev100 Oct-1999 #cont_change 15-Oct-1999
 R: Jensen, M.; Lemaire, N.; Quail, M.; Harris, B.; Rajadurai, M.A.; Barrall, B.G.; Banerjee, submitted to the Protein Sequence Database, August 1999
 A reference: T21315
 A molecule type: DNA
 A residues: 1-988

 A description: BMDA110819
 A experimental source: Cultivar Columbia; BAC clone T7805
 C identifier:
 A gene: AT5G7805.30
 A map position: 31, 201/3, 416/3, 438/3, 460/3, 482/3, 504/3, 519/3, 534/3, 559/3, 579/3;
 C superfamily: Arabidopsis thaliana hypothetical protein T2C14.40

Query Match 10.8% Score 96.5; DB 2; Length 871;
 Best local similarity 25.0%; Pred. No. 21;
 Matches 45; Conservative 31; Mismatches 63; Indels 39; Gaps 8

9 KATVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 52
 Db KATVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 695
 63 K---KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 114
 Db KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 174
 699 KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 174
 751 KQGVSEELP---HATVATYQKQKSTVSEEDPIPLVYKCEK-----DTQKISGPRGKQAGVYKSLR 808

RESULT 24
 C97267
 hypothetical protein C97267 (Imported) - Clostridium acetobutylicum

[illegible]

GenCore version 5.1.6
(c) 1993 - 2004 CompuGen Ltd.

Copyright (c) 1993 - 2004

OM protein - protein search, using SW model

Run on: February 10, 2004, 10:48:45 ; Search time 11.8417 Seconds

1331.870 Million cell updates/sec

Title: US-10-067-385-8_COPY_610_773

Sequence: 1 ITVKEPILNKDGEVSELKP.....ATVLDKNNISSKSTNNPNK 164

scoring table: BLOSUMPz
Gapen 10 0 - Gapext 0 5

Searched: 203308 RECD. 96168682 F

Total number of bites satisfying chosen parameter

Minimum DB seq length: 0

00000007 : 1986-08-25

Maximum Match 10

100

1: π_1 =

3: **pl r3: ***

Prod No 49-48a-011

score greater than 10 and is derived by a

Result	Query
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
23	23
24	24
25	25
26	26
27	27
28	28
29	29
30	30
31	31
32	32
33	33
34	34
35	35
36	36
37	37
38	38
39	39
40	40
41	41
42	42
43	43
44	44
45	45
46	46
47	47
48	48
49	49
50	50
51	51
52	52
53	53
54	54
55	55
56	56
57	57
58	58
59	59
60	60
61	61
62	62
63	63
64	64
65	65
66	66
67	67
68	68
69	69
70	70
71	71
72	72
73	73
74	74
75	75
76	76
77	77
78	78
79	79
80	80
81	81
82	82
83	83
84	84
85	85
86	86
87	87
88	88
89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

Figure 6.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	Db ID	Description
1	88.8	100.0	2140	219504
2	88.8	100.0	2140	219504
3	88.8	100.0	2140	219504
4	110	113.0	1038	219504
5	106	113.0	559	219504
6	106	113.0	559	219504
7	103.5	112.2	328	219504
8	101.5	112.0	312	219504
9	99.5	111.7	368	219504
10	99.5	111.7	368	219504
11	99	111.7	211	219504
12	97.9	111.7	219	219504
13	97.9	111.7	219	219504
14	97.5	114.5	136	219504
15	97	114.5	988	219504
16	96.5	114.5	988	219504
17	96.5	114.5	988	219504
18	96	111.3	2800	219504
19	95.5	111.3	644	219504
20	95	111.3	139	219504
21	95	111.3	139	219504
22	94.5	111.1	867	219504
23	94.5	111.1	867	219504
24	94.5	111.1	867	219504
25	94.5	111.1	210	219504
26	93.5	111.0	645	219504
27	93.5	111.0	645	219504
28	93	111.0	246	219504
29	93	111.0	246	219504

[illegible]


```
Db      924 TSNNREKIDIRNRSKTIODPSHSYIND-KKELRWYASQNNWTDNQTAKIR 982
Qy      73 QVYNLSOTPIKVPFKIERKKZSNPTDVSKKQONVQNSQJNSHREDJQEE 132
Db      983 IT--NLLKNNKIKKIDWAKVATIDLER-----NKKKNMNSHKKITQJNSJAK 1035
Qy      133 HGGQSDSTO-----VATLDNNIS 155
Db      1048 CCKKIKSTIDNPSKCIKNTIKLTKTIVKNNKLT 1072
```

Search completed: February 10, 2004, 10:58:35
Job time : 12.8417 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 10:48:44 / Search time 29.0166 seconds

1597493 Million cell updates/sec

Title: US-10-067-385-8_COPY_610_773

Sequence score: 848

Perceptron: 1

Scoring table: BL080W62

Gapop 10.0, Gapcut 0.5

Search: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing time: 45 minutes

Database: 1: SPRED01_23*

2: sp_bacteria*

3: sp_fungi*

4: sp_human*

5: sp_mammalia*

6: sp_mammalia*

7: sp_mhi*

8: sp_organella*

9: sp_plant*

10: sp_protista*

11: sp_protista*

12: sp_virus*

13: sp_virus*

14: sp_virus*

15: sp_virus*

16: sp_bacteriophage*

17: sp_archaeum*

RESULTS

Pred. No. in the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	848	100.0	2119	2	Q9435 streptococ
2	848	100.0	2119	16	Q9435 streptococ
3	848	99.5	2144	16	Q9435 streptococ
4	848	99.5	2144	16	Q9435 streptococ
5	119	14.0	775	16	Q9435 streptococ
6	112.5	13.3	361	5	Q9435 streptococ
7	112.5	13.3	361	5	Q9435 streptococ
8	112.5	13.3	361	5	Q9435 streptococ
9	111.5	13.1	354	5	Q9435 streptococ
10	111.5	13.1	354	5	Q9435 streptococ
11	111.5	13.1	354	5	Q9435 streptococ
12	110.5	13.0	329	5	Q9435 streptococ
13	110.5	13.0	329	5	Q9435 streptococ
14	110.5	13.0	329	5	Q9435 streptococ
15	109.5	12.9	380	5	Q9435 streptococ
16	109.5	12.9	380	5	Q9435 streptococ

17	109	12.9	3008	5	Q81436 plasmodium
18	108.5	12.8	600	5	Q77355 plasmodium
19	107.5	12.7	470	10	Q93939 plasmodium
20	106.5	12.5	324	5	Q93939 plasmodium
21	106.5	12.5	324	5	Q93939 plasmodium
22	104	12.3	540	10	Q94C59 plasmodium
23	104	12.3	540	10	Q94C59 plasmodium
24	103.5	12.2	248	5	Q94B44 plasmodium
25	102.5	12.1	238	5	Q94B44 plasmodium
26	102.5	12.1	238	5	Q94B44 plasmodium
27	101.5	12.0	312	16	Q93P15 plasmodium
28	101.5	12.0	312	16	Q93P15 plasmodium
29	101.5	12.0	312	16	Q93P15 plasmodium
30	101.5	12.0	312	16	Q93P15 plasmodium
31	101.5	12.0	312	16	Q93P15 plasmodium
32	100.5	11.9	312	16	Q93P15 plasmodium
33	100.5	11.9	312	16	Q93P15 plasmodium
34	100.5	11.9	312	16	Q93P15 plasmodium
35	100	11.8	622	16	Q94Q24 plasmodium
36	100	11.8	622	16	Q94Q24 plasmodium
37	99.5	11.7	3185	5	Q94124 plasmodium
38	99.5	11.7	3185	5	Q94124 plasmodium
39	99.5	11.7	3185	5	Q94124 plasmodium
40	99	11.7	211	5	P91466 plasmodium
41	99	11.7	211	5	P91466 plasmodium
42	99	11.7	211	5	P91466 plasmodium
43	99	11.7	211	5	P91466 plasmodium
44	99	11.7	211	5	P91466 plasmodium
45	99	11.7	211	5	P91466 plasmodium

ALIGNMENTS

RESULT 1

ID Q9435 PRELIMINARY: PRT, 2119 AA.

NC 01-JUN-2001 (TRENDEL, 17, Created)

PT 01-JUN-2001 (TRENDEL, 17, Last annotation update)

PT 01-JUN-2001 (TRENDEL, 23, Last annotation update)

DB Streptococcus pneumoniae

OC Streptococcus pneumoniae

CC Streptococcus pneumoniae

NC 01-JUN-2001 (TRENDEL, 17, Created)

PT 01-JUN-2001 (TRENDEL, 17, Last annotation update)

PT 01-JUN-2001 (TRENDEL, 23, Last annotation update)

DB Streptococcus pneumoniae

OC Streptococcus pneumoniae

CC Streptococcus pneumoniae

NC 01-JUN-2001 (TRENDEL, 17, Created)

PT 01-JUN-2001 (TRENDEL, 17, Last annotation update)

PT 01-JUN-2001 (TRENDEL, 23, Last annotation update)

DB Streptococcus pneumoniae

OC Streptococcus pneumoniae

CC Streptococcus pneumoniae

NC 01-JUN-2001 (TRENDEL, 17, Created)

PT 01-JUN-2001 (TRENDEL, 17, Last annotation update)

PT 01-JUN-2001 (TRENDEL, 23, Last annotation update)

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Complan Ltd.

OM protein - protein search using sw model

Run on: February 10, 2004, 10:48:44 | Search time 35.036 Seconds
(without alignments)
697.707 Million cell updates/sec

US-10-067-385-8_COPY_620_773

Title: DTGSSEKKEKRYVLTQNG.....ATTNDNNISSTSTPNRK 134

Sequence: 1 DTGSSEKKEKRYVLTQNG.....ATTNDNNISSTSTPNRK 134

Scoring table: DTGSSEKKEKRYVLTQNG.....ATTNDNNISSTSTPNRK 134

Depos 10.0 - Depact 0.5

Searched: 110763 seqs, 13872673 residues

Total number of hits satisfying chosen parameters: 110763

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Filtering filter: 0% similarities

Database:

1. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1910.DMT*
2. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DMT*
3. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DMT*
4. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DMT*
5. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DMT*
6. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DMT*
7. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DMT*
8. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DMT*
9. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DMT*
10. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DMT*
11. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DMT*
12. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DMT*
13. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DMT*
14. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DMT*
15. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DMT*
16. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DMT*
17. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DMT*
18. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DMT*
19. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DMT*
20. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DMT*
21. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DMT*
22. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DMT*
23. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DMT*
24. /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DMT*

Prd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMILARITIES

Result No.	Score	Match	Length	DB	ID	Description
1	799	100.0	773	22	AA68343	S. pneumoniae Sp13
2	799	100.0	2140	24	AA80370	Streptococcus pneumoniae
3	799	100.0	2140	24	AA80370	Streptococcus pneumoniae
4	799	100.0	2140	24	AA80370	Streptococcus pneumoniae
5	615	77.0	117	23	AA85590	S. pneumoniae Sp94
6	615	77.0	146	22	AA85590	S. pneumoniae Sp94
7	118	14.8	778	23	AA85903	S. epidermidis spe
8	103	13.3	665	21	AA81278	Streptococcus pneumoniae
9	103	13.3	665	21	AA81278	Streptococcus pneumoniae

10	101.5	12.7	564	22	AA86197	Drosophila melanogaster
11	96.5	12.1	2560	21	AA81272	Streptococcus pneumoniae
12	96.5	12.1	2560	21	AA81272	Streptococcus pneumoniae
13	93.5	11.7	408	21	AA63714	Arabidopsis thaliana
14	93.5	11.7	456	21	AA63714	Arabidopsis thaliana
15	93.5	11.7	2416	22	AA63714	Arabidopsis thaliana
16	93.5	11.7	2416	22	AA63714	Arabidopsis thaliana
17	90.5	11.3	209	21	AA442897	Human ORF ORF661
18	90.5	11.3	757	21	AA443364	Human cell cycle
19	90.5	11.3	428	21	AA43180	Streptococcus pneumoniae
20	90.5	11.3	428	21	AA43180	Streptococcus pneumoniae
21	90.5	11.3	428	21	AA43180	Streptococcus pneumoniae
22	90.5	11.3	654	24	AA856879	Streptococcus pneumoniae
23	90.5	11.3	1183	22	AA856879	Streptococcus pneumoniae
24	89.5	11.2	511	20	AA735091	Chlamydia pneumoniae
25	89.5	11.2	525	20	AA735091	Chlamydia pneumoniae
26	89.5	11.2	525	20	AA735091	Chlamydia pneumoniae
27	89.5	11.2	1408	22	AA856879	Streptococcus pneumoniae
28	88.5	11.1	881	22	AA856879	Streptococcus pneumoniae
29	88.5	11.1	881	22	AA856879	Streptococcus pneumoniae
30	88.5	11.1	1141	22	AA856879	Streptococcus pneumoniae
31	88.5	11.1	1141	22	AA856879	Streptococcus pneumoniae
32	88.5	11.1	225	23	AA856879	Streptococcus pneumoniae
33	88.5	11.1	817	22	AA735118	Human protein S80
34	88.5	11.1	817	22	AA735118	Human protein S80
35	87.5	11.0	2515	22	AA80269	Human protein S80
36	87.5	11.0	2515	22	AA80269	Human protein S80
37	87.5	11.0	2515	22	AA80269	Human protein S80
38	87.5	11.0	2515	22	AA80269	Human protein S80
39	87.5	11.0	3021	24	AA856879	Streptococcus pneumoniae
40	87.5	11.0	3021	24	AA856879	Streptococcus pneumoniae
41	87.5	11.0	3021	24	AA856879	Streptococcus pneumoniae
42	87.5	11.0	3021	24	AA856879	Streptococcus pneumoniae
43	87.5	11.0	3021	24	AA856879	Streptococcus pneumoniae
44	87.5	11.0	3021	24	AA856879	Streptococcus pneumoniae
45	86.5	10.8	443	22	AA856879	Streptococcus pneumoniae

ALIGNMENTS

RESULT 1
ID: AA68343 standard; Protein: 773 AA.
AC: AA68343
XX 20-APR-2001 (first entry)
DE: S. pneumoniae Sp13 polypeptide.
KW: Immunogenic; Sp13; pneumoniae; otitis media; nasopharyngeal;
KW: bronchial; lung; blood; infection; immune response; immunotherapy;
KW: antibacterial; adjuvant; vaccine.
XX Streptococcus pneumoniae.
XX W0200076540-X2.
XX 21-DEC-2000.
XX 09-JUN-2000; 200000-US15925.
XX 10-JUN-1999; 99US-0138453.
XX (MED1-) MED TOWNS INC.
XX Adamou JE, Choi GH;
XX WPI, 2001-11/17/12.
XX R-PSDB; MDS1742.
XX New vaccines comprising Sp128 or Sp130 polypeptides, for treating and

[illegible]

[illegible]

[illegible][illegible]

CC the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include (a) infectious diseases, (b) chronic inflammatory conditions (e.g. asthma or arthritis), (c) proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischemia, bone disorders (e.g., osteoporosis), and abnormal bone growth, (d) cancer, (e) neurodegenerative diseases, (f) cystic fibrosis, (g) viral infections, (h) autoimmune diseases, (i) wound healing (e.g., of burns, lacerations and ulcers), while those with (j) immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections. Polypeptides may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to stimulate stem cells in culture to give rise to neuroepithelial cells that can be used to replace cells damaged by disease. Polypeptides may also be used to stimulate the proliferation of cells. Polypeptides may also be used in the diagnosis of the above conditions and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.

Sequence 2515 AA:

Query Match 11.0% Score 87.5; DB 22; Length 3515;

Matches 38; Conservative 29; Mismatches 55; Indels 35; Gaps 6;

5 VSELEKRNATVQKNSSTVSEEDFLPYVKEGLKNGTQDKEISFGDQKGY 64

2352 IADLQGRFLVMSLWNSPTNIEHSPTNGELISGKNNKASISGVAD-- 2409

65 VYLSKNTFTFKPYKKLKKXKXENKPTFVDSK--DNQVNSQLNESH 113

2410 -----KSTF--SRHMK--RKGQTLSEDESDPNVPLDST-ET 2449

114 KSDQGRHSQNSSTQVATVADNKNISSTNT 150

2450 GRCCTPRHAKVKNQSDLR--LRTSSTNTS 2484

114 KSDQGRHSQNSSTQVATVADNKNISSTNT 150

AA080268 standard; Protein: 2515 AA.

AA080268 (first entry)

06-NOV-2001

Human protein SEQ ID NO 3914.

Human: cytokine; cell proliferation; cell differentiation; gene therapy;

tissue growth factor; immunomodulatory; cancer; leukemia;

nervous system disorder; arthritis; inflammation.

Homo sapiens.

WC000157130-42.

09-AUG-2001.

05-FEB-2001. 2001.NC-US94098.

03-FEB-2000. 2000US-0496914.

20-JUN-2000. 2000US-0548875.

19-JUL-2000. 2000US-0620325.

01-SEP-2000. 2000US-0654936.

15-SEP-2000. 2000US-0663152.

20-JUN-2000. 2000US-0558875.

30-NOV-2000. 2000US-0728422.

(HRS-) HRSBQ INC.

E1 Tang YZ, Liu C, Dmanec RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y, P1 Zuo QH, Wang D, Wang Y, Zhang Y, Ren P, Chen R, Wang ZW, X1 Xie M, Tang Y, Weinman T, Goodrich R, DR N-5008; AAK53401.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.

NCBI: 2001-047883/51.


```

PR 20-ANG-1999 99US-0149723
PR 20-ANG-1999 99US-0149929
PR 23-ANG-1999 99US-0149902
PR 23-ANG-1999 99US-0149900
PR 23-ANG-1999 99US-0149900
PR 26-ANG-1999 99US-0150884
PR 26-ANG-1999 99US-0150884
PR 27-ANG-1999 99US-0151065
PR 27-ANG-1999 99US-0151066
PR 27-ANG-1999 99US-0151066
PR 30-ANG-1999 99US-0151303
PR 31-ANG-1999 99US-0151438
PR 01-SEP-1999 99US-0153900
PR 07-SEP-1999 99US-0153900
PR 10-SEP-1999 99US-0153070
PR 13-SEP-1999 99US-0153788
PR 15-SEP-1999 99US-0154018
PR 15-SEP-1999 99US-0154018
PR 20-SEP-1999 99US-0154779
PR 22-SEP-1999 99US-0155119
PR 23-SEP-1999 99US-0155466
PR 23-SEP-1999 99US-0155466
PR 28-SEP-1999 99US-0156458
PR 29-SEP-1999 99US-0156596
PR 04-OCT-1999 99US-0157117
PR 04-OCT-1999 99US-0157117
PR 06-OCT-1999 99US-0157865
PR 07-OCT-1999 99US-0158029
PR 08-OCT-1999 99US-0158222
PR 08-OCT-1999 99US-0158222
PR 12-OCT-1999 99US-0159293
PR 13-OCT-1999 99US-0159284
PR 13-OCT-1999 99US-0159295
PR 13-OCT-1999 99US-0159295
PR 14-OCT-1999 99US-0159310
PR 14-OCT-1999 99US-0159310
PR 14-OCT-1999 99US-0159637
PR 14-OCT-1999 99US-0159637
PR 14-OCT-1999 99US-0159644
PR 21-OCT-1999 99US-0160741
PR 21-OCT-1999 99US-0160741
PR 21-OCT-1999 99US-0160747
PR 21-OCT-1999 99US-0160770
PR 21-OCT-1999 99US-0160814
PR 21-OCT-1999 99US-0160815
PR 22-OCT-1999 99US-0160981
PR 22-OCT-1999 99US-0160981
PR 22-OCT-1999 99US-0160989
PR 25-OCT-1999 99US-0161404
PR 25-OCT-1999 99US-0161405
PR 25-OCT-1999 99US-0161406
PR 26-OCT-1999 99US-0161359
PR 26-OCT-1999 99US-0161360
PR 26-OCT-1999 99US-0161361
PR 26-OCT-1999 99US-0161361
PR 28-OCT-1999 99US-0161992
PR 28-OCT-1999 99US-0161993
PR 29-OCT-1999 99US-0162142

```

Query March

10.9% Score 87; DB 21; Length 113;

Best Local

Similarity 25.4%; Pred. No. 2.5;

Matches

36; Conservative 26; Mismatches 46; Indels 34; Gaps 6;

```

QY      6  SELLKPRVYVTCQKNGSTVREDPIYTKGELKXVCFQPMISG-PPQNDQW 64
DB      55  SSKNNR--KXJGKELIS-----PAG-KLSKKKKKNGV 91
QY      65  VINSJDFKPKVKKLEKKKKENPTDQSKCKNPOVNSQLMSHPEDLOEHS 124
DB      92  NVDISPVLALSTERYKKKKKKKK--TKKKKKASITSSV-----EDKSESTF 141
QY      125  QKNSSTGYVATLQNDKSK 146
DB      142  KSNKKKKKKKKKKKKKKKKKK 163

```


Oy 49 KEELENGVQDQNHISGFEKQDAVYINSLDTIEFVFKLIEKCEBENKPTF--Dy 105
 Db 205 KEELENGVQDQNHISGFEKQDAVYINSLDTIEFVFKLIEKCEBENKPTF--Dy 105
 Oy 106 SV--KCCNVNYSVQDA--SHKNDQVQREBSVQSTQ--VATVADLVNNT 133
 Db 257 SHKNDQVQREBSVQSTQ--VATVADLVNNT 133
 Oy 154 SSK 156
 Db 314 SSK 316
 RESULT 4
 ID TOP2 PLAKR STANDARD PRF, 1398 M.
 AC P41001.
 DT 01-FEB-1995 (Reg. 31, Created)
 DT 20-MAY-2000 (Reg. 33, Last annotation update)
 DE DNA topoisomerase II (EC 5.99.1.3).
 DN TOP2-ecellul topoisomerase (isolated from *Drosophila*)
 CC Bacteroides Alveolaris, Apicomplexa, Hemaphyspida, Plasmodium.
 CX NCBI Taxid=8839.
 SR MEDLINE=94116596; PubMed=8901616;
 RA Chiemman S., McInnes S., Goman M., Johnson D., Horrocks P.,
 Ridley R.G., Kibbey B.J.;
 RT Nucleic Acids Res. 27:11934-11944 (1999).
 CC -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSDUCING
 BREAKAGES AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPISOMERASE II
 CATALYZES THE BREAKAGE AND REJOINING OF DNA STRANDS.
 CC -1- CATALYZES THE BREAKAGE AND REJOINING OF DNA STRANDS.
 CC -1- of double-stranded DNA, -dependent breakage, passage and rejoining
 CC -1- SUBSTRATE: Homodimer (By similarity).
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
 CC This SWISS-PROT entry is copyright © it is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL, operation -
 the European Bioinformatics Institute. There are no restrictions on its
 use, modification or distribution. It is made available under a Creative
 Commons Attribution 3.0 license. For more information, see the Creative
 Commons Attribution 3.0 license agreement (see <http://www.embnet.org/licenses/CC-BY-3.0/>)
 or send an email to license@ebi.ac.uk.
 DR EMBL: X79345; 1. NOT ANNOTATED; CDS
 DR HSPB: P06786; 18CM
 DR InterPro: IPR003534; ATPbind, ATPase.
 DR InterPro: IPR001537; GTPase, NTPase.
 DR InterPro: IPR002085; DNA_topoisom.
 DR Pfam: PF00294; DNA_gyraseB; 1.
 DR Pfam: PF00241; DNA_topoisom; 1.
 DR PRINTS: PR00615; CATALYTIC.
 DR PRINTS: PR00418; TYP2PMTLY.
 DR SMART: SM00382; DNA_topoisom; 1.
 DR SMART: SM00433; T02c2; 1.
 DR SMART: SM00433; T02c2; 1.
 DR PROSITE: PS00077; ATPbind; 1.
 DR PROSITE: PS00077; ATPbind; 1.
 DR ACT_SITE 830 830 ATP (CONTINGUALLY).
 DR ACT_SITE 830 830 POLY-AMN.
 DR DOMAIN 208 316

PF DOMAIN 1089 1093 POLY-LIG.
 SQ SEQUENCE 1398 M; 161029 MW; BAA07088672889 CCKC4;
 Oy Query Match 11.2%; Score 95; DB 1; Length 649;
 Db Beat Local 36; Conservative 36; Mismatch 53; Indels 26; Gaps 6;
 Oy 29 NQKNSVSTVSEEDPTL--PYVSGSLKQVQDQNHISGFEKQDAVYINSLDTIEFVFKLIEKCEBENKPTF--Dy 105
 Db 1133 NQKNSVSTVSEEDPTL--PYVSGSLKQVQDQNHISGFEKQDAVYINSLDTIEFVFKLIEKCEBENKPTF--Dy 105
 Oy 87 VFKKSL--KKEBKNKPTPVYSGSLKQVQDQNHISGFEKQDAVYINSLDTIEFVFKLIEKCEBENKPTF--Dy 105
 Db 1190 VFKKSL--KKEBKNKPTPVYSGSLKQVQDQNHISGFEKQDAVYINSLDTIEFVFKLIEKCEBENKPTF--Dy 105
 Oy 136 ---KEDSTVATVADLVNNTSSKSTTNNY 163
 Db 1243 GQDSTVATVADLVNNTSSKSTTNNY 1273
 RESULT 5
 ID TOP2 PLAKR STANDARD PRF, 649 M.
 AC P37839.
 DT 01-OCT-1994 (Reg. 30, Created)
 DT 20-MAY-2000 (Reg. 33, Last annotation update)
 DE Heat shock 70 kDa protein.
 DN HSP70.
 CC Pyrenomonas salina.
 CC Bacteroides Alveolaris, Apicomplexa, Hemaphyspida, Plasmodium.
 CX NCBI Taxid=1034.
 SR MEDLINE=94458506; PubMed=8208251;
 RA Hofmann C.J.B., Remington S.A., Heuvel M.M., Martin M.F., Mueller S.B.,
 Cohen J., Weidman G.T., Fogel G.L., Malar U.-G.;
 RT Nucleic Acids Res. 27:11934-11944 (1999).
 CC -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSDUCING
 BREAKAGES AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPISOMERASE II
 CATALYZES THE BREAKAGE AND REJOINING OF DNA STRANDS.
 CC -1- CATALYZES THE BREAKAGE AND REJOINING OF DNA STRANDS.
 CC -1- of double-stranded DNA, -dependent breakage, passage and rejoining
 CC -1- SUBSTRATE: Homodimer (By similarity).
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
 CC This SWISS-PROT entry is copyright © it is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL, operation -
 the European Bioinformatics Institute. There are no restrictions on its
 use, modification or distribution. It is made available under a Creative
 Commons Attribution 3.0 license. For more information, see the Creative
 Commons Attribution 3.0 license agreement (see <http://www.embnet.org/licenses/CC-BY-3.0/>)
 or send an email to license@ebi.ac.uk.
 DR EMBL: X79345; 1. NOT ANNOTATED; CDS
 DR HSPB: P06786; 18CM
 DR InterPro: IPR003534; ATPbind, ATPase.
 DR InterPro: IPR001537; GTPase, NTPase.
 DR InterPro: IPR002085; DNA_topoisom.
 DR Pfam: PF00294; DNA_gyraseB; 1.
 DR Pfam: PF00241; DNA_topoisom; 1.
 DR PRINTS: PR00615; CATALYTIC.
 DR PRINTS: PR00418; TYP2PMTLY.
 DR SMART: SM00382; DNA_topoisom; 1.
 DR SMART: SM00433; T02c2; 1.
 DR PROSITE: PS00077; ATPbind; 1.
 DR PROSITE: PS00077; ATPbind; 1.
 DR ACT_SITE 830 830 ATP (CONTINGUALLY).
 DR ACT_SITE 830 830 POLY-AMN.
 DR DOMAIN 208 316

FT	DNAI1	59	294	(POTENTIAL)
PT	DNAI1	59	294	EXTRACELLULAR (POTENTIAL).
CC	DNAI1	59	294	TRANSMEMBRANE.
PT	DNAI1	329	662	TRANSPOSITIONS.
PT	DNAI1	706	784	FIBROBLAST TYPE-III.
PT	ACT SITE	300	350	ACTIN-BINDING SITE.
CC	SERpinase	914-941	99562 MW,	ACTIVATED BY PASCILLULIN (BY SIMILARITY).
CC	SERpinase			CYTOPLASMIC PROTEIN IN CYCLOPS.
QY	Query Match	10.1%	Score 86;	DB 1; Length 914;
BT	Best Local Similarity:	23.0%;	Freqd. No. 49;	
MC	Matches	45	Conservative	351 Mismatches
QY	3	VPEPFLVIAAGGVELEKAVHVVITVDTGGDNGSTVISEDETVLVYVKEISGLRGTQPDHNE	62	GAPG
DB	737	WASV...DGSFSE...--LHNS--KAAHLSGVGVSV--NTERVA	774	
QY	63	LSPEDKKDA-CGYVALKNPTVLPVYVKIKESKSEN...	100	
DB	773	VSD-DVSLSSLEIVYKALHEDKDDQQQVVDGADKDQKQVQTGDQDQDQDQDQD	830	
QY	101	--PFVFKKKDKDNQVYHSQVLA--EENKRGDQHEHSQDSDETPAYIA	145	
DB	834	QTDGNDNQDQKQDQNVTHVFNHNQDQSHNDQNDQNDQDQSQRNDQSTO-SD	891	
QY	146	TVLVDNNLSKSKTNN	161	
DB	892	TNNNTCTSKTKTNS	907	
RESULT 23				
MC	HUMAN	STANDARD;	PRF:	5596 AA.
AD	Q9NRJ2: 015013	Created:		
DT	28-FEB-2003	(Rel. #1, Created)		
DT	28-FEB-2003	(Rel. #1, Last sequence update)		
DT	28-MAR-2003	(Rel. #1, Last sequence update)		
DR	NCBI	GenBank		
GN	KOM1 OR KIA00101.			
OS	Homo sapiens (human)			
CS	Nucleoside diphosphate synthetase			
CK	Kom1 protein; Primase; Geminin; Cerebellin; Homidase; Hono.			
CK	NCBI_Tatbin=8696;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RA	Garbarino J.R., Gilbohn I.R.;			
EX	Published=12102729.			
RT	Expression and genomic analysis of midasin, a novel and highly			
EL	BMC Genomics 3:18-18(2002).			
RP	[2]			
RA	SEQUENCE OF 1285-2356 AND 3550-5596 FROM N.A.			
RA	T15509=GenPept;			
RA	Submitted (Apr-2000) to the EMBL/Genbank/DDBJ database.			
RP	[3]			
RA	SEQUENCE OF 3550-5596 FROM N.A.			
EX	MEDLINE=D91319941; PubMed=9205541;			
RA	Nagata T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,			
RA	Miyajima N., Tanaka A., Kozumi H., Nomura N., Obara O.			
RT	The complete sequences of 160 new cDNA clones from brain which can			
RL	code for large proteins in vitro?			
DL	DATA Row. 4:14-150(1997).			
CC	-I-			
CC	the assembly/disassembly of macromolecular complexes in the			
CC	nucleus.			
CC	-II-			
CC	SUBCELLULAR LOCATION: Nucleus (by similarity).			
CC	-III-			
CC	SIMILARITY: Contains 1 WRM domain.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL, integration -			


```

Query Match          9.84; Score 83; DB 1; Length 715;
Best Local Similarity 23.14; Pred. No. 62;
Matches 36; Conservative 30; Mismatches 47; Indels 36; Gaps 5;

Qv      22 RVTYTLONGKSGSTIVSRHDTLPVYKGLKGVQFOCMELISQPEK-----KMGTV 75
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      262 RVTVALEENPFSKQMLISRECTILD--HAAKQITVWKGDNVQKQKAAKTAERFAQ 319
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qv      76 INLSKDTIK-----PVPFK-----IEKKERENKPTFVSKCK 109
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      320 KATNSNTQIQVLPESCEETLPKQPTQMRDQDSQFQNTVYTERAKQIQIPDASLKH 379
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qv      110 DNRQV--NHSQLEHREKEDLQREHS 134
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      380 SSKQALQSHRPVDDSGSKREIWRVENN 406
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: February 10, 2004, 10:49:55
 Job time : 9.62413 secs

GenCode version 5.1.6
Copyright (c) 1995 - 2004 Comagen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 10:48:44 Search time 8.0892 Seconds

(without alignments) 101.574 Million call updates/sec

Title: US-10-067-385-8_COPY_600_773

Perfect score: 897

Sequence: 1 KLVQDPAKNTVFATLAK.....ATVDNNISSTQNPVK 174

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47082705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0

Listing files as summaries

Database: SwissProt_41.1

Pred. No. is the number of families predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
	1	100	11.1	1875	1	MLP1_YEAST	Q02455 saccharomy
	2	99	11.0	1398	1	TOP2_PARK	P10011 plasmidom
	3	97.5	10.9	1349	1	THO2_YEAST	P18800 saccharom
	4	97.0	10.7	1281	1	GRM1_YEAST	P14112 saccharom
	5	96.6	10.7	893	1	GRM1_STRAP	P14112 saccharom
	6	95	10.6	1202	1	DPW1_YEAST	P22274 saccharom
	7	93.3	10.4	1202	1	DPW1_YEAST	P22274 saccharom
	8	93.3	10.4	1202	1	DPW1_YEAST	P22274 saccharom
	9	93.3	10.4	1202	1	DPW1_YEAST	P22274 saccharom
	10	93	10.4	1202	1	DPW1_YEAST	P22274 saccharom
	11	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	12	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	13	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	14	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	15	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	16	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	17	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	18	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	19	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	20	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	21	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	22	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	23	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	24	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	25	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	26	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	27	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	28	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	29	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	30	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	31	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	32	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	33	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom

Result	No.	Score	Match	Length	DB	ID	Description
	34	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	35	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	36	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	37	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	38	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	39	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	40	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	41	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	42	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	43	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	44	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	45	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	46	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	47	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	48	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	49	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom
	50	85.5	9.5	1007	1	ROA1_YEAST	P19088 saccharom

ALIGNMENTS

Result	No.	Score	Match	Length	DB	ID	Description
	1	100	11.1	1875	1	MLP1_YEAST	Q02455 saccharom
	2	99	11.0	1398	1	TOP2_PARK	P10011 plasmidom
	3	97.5	10.9	1349	1	THO2_YEAST	P18800 saccharom
	4	97.0	10.7	1281	1	GRM1_YEAST	P14112 saccharom
	5	96.6	10.7	893	1	GRM1_STRAP	P14112 saccharom
	6	95	10.6	1202	1	DPW1_YEAST	P22274 saccharom
	7	93.3	10.4	1202	1	DPW1_YEAST	P22274 saccharom
	8	93.3	10.4	1202	1	DPW1_YEAST	P22274 saccharom
	9	93.3	10.4	1202	1	DPW1_YEAST	P22274 saccharom
	10	93	10.4	1202	1	DPW1_YEAST	P22274 saccharom
	11	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	12	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	13	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	14	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	15	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	16	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	17	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	18	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	19	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	20	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	21	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	22	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	23	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	24	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	25	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	26	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	27	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	28	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	29	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	30	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	31	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	32	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom
	33	92.5	10.3	1443	1	WAP1_YEAST	P18800 saccharom

Genome version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 10:48:44 / Search time 37.396 seconds

(ELCUT alignment 697.707 Million cpi updates/sec

Title: US-10-067-385-8_COPY_610_773

Perfect score: 848

Sequence: 1 TTAKETFLMNDTGRSLR.....ATTYNNKISSTSRPNRK 164

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 1107863 seqs, 15076577 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 300000000

Post processing: Minimum Match 0.0

Listing first 45 summaries

Database: A_Genome_130jun03.*

1: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11980.DMT.*

2: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11981.DMT.*

3: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11982.DMT.*

4: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11983.DMT.*

5: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11984.DMT.*

6: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11985.DMT.*

7: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11986.DMT.*

8: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11987.DMT.*

9: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11988.DMT.*

10: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11989.DMT.*

11: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11990.DMT.*

12: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11991.DMT.*

13: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11992.DMT.*

14: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11993.DMT.*

15: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11994.DMT.*

16: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11995.DMT.*

17: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11996.DMT.*

18: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11997.DMT.*

19: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11998.DMT.*

20: /SID01/5cgcata/Geneseg/Geneseg-emb1/A11999.DMT.*

21: /SID01/5cgcata/Geneseg/Geneseg-emb1/A12000.DMT.*

22: /SID01/5cgcata/Geneseg/Geneseg-emb1/A12001.DMT.*

23: /SID01/5cgcata/Geneseg/Geneseg-emb1/A12002.DMT.*

24: /SID01/5cgcata/Geneseg/Geneseg-emb1/A12003.DMT.*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	848	100.0	773	22	AA048343	S. pneumoniae Sp13
2	848	100.0	2120	21	AA017110	S. pneumoniae Sp13
3	848	100.0	2140	24	AB001020	S. pneumoniae type
4	848	100.0	2140	24	AB001020	S. pneumoniae type
5	613	72.5	117	23	AB045590	S. pneumoniae Sp04
6	119	14.0	746	22	AA081779	S. pneumoniae type
7	119	14.0	778	23	AB034023	Staphylococcus epi
8	10706	12.5	665	21	AA018278	Pseudomonas faulpii

10	101.5	13.0	564	23	AB054137	Drosophila melanog
11	99.5	11.7	1384	24	AB055413	Human HMD-2 proc
12	99.5	11.7	1404	24	AB055393	Human KUD-2 proc
13	97.5	11.5	2519	22	AB016436	Novel human diapo
14	96.5	11.4	456	21	AA037133	Arabidopsis thalia
15	96.5	11.4	476	21	AA037132	Arabidopsis thalia
16	96.5	11.4	476	21	AA037132	Arabidopsis thalia
17	96.5	11.4	2660	23	AB120967	Staphylococcus lug
18	93.9	11.0	2500	24	AA131062	Staphylococcus epi
19	93.5	11.0	654	24	AB054879	Staphylococcus epi
20	93.5	11.0	654	24	AB054879	Staphylococcus epi
21	92.5	10.9	645	24	AB181979	Staphylococcus epi
22	92.5	10.8	309	22	AB044322	Staphylococcus epi
23	91.5	10.7	442	23	AB031468	Staphylococcus epi
24	91.5	10.7	442	23	AB031468	Staphylococcus epi
25	90.5	10.7	902	23	AB049312	Staphylococcus epi
26	90.5	10.7	409	21	AB041997	Human OMT2A63
27	90.5	10.7	409	21	AB041997	Human OMT2A63
28	90.5	10.7	757	21	AA044364	Human cell cycle
29	90.5	10.7	758	21	AB053119	Human colon cancer
30	90.5	10.7	901	23	AB069363	Human polypeptide
31	89.5	10.6	511	20	AA035091	Staphylococcus epi
32	89.5	10.6	511	20	AA035091	Staphylococcus epi
33	89.5	10.6	402	20	AA001390	S. aureus triger
34	89.5	10.6	1408	22	AB059704	S. aureus triger
35	89.5	10.6	525	20	AA001869	S. aureus triger
36	89.5	10.6	525	20	AA001869	S. aureus triger
37	89.5	10.6	1408	22	AB059704	S. aureus triger
38	89.5	10.5	296	23	AB059341	Staphylococcus epi
39	89.5	10.5	296	23	AB059341	Staphylococcus epi
40	88.5	10.4	141	23	AA058008	Staphylococcus epi
41	88.5	10.4	225	23	AB073992	Staphylococcus epi
42	88.5	10.4	225	23	AB073992	Staphylococcus epi
43	88.5	10.4	225	23	AB073992	Staphylococcus epi
44	88.5	10.4	225	23	AB073992	Staphylococcus epi
45	88.5	10.4	225	23	AB073992	Staphylococcus epi

ALIGNMENTS

1	AA048343	standard; Protein: 773 AA.
2	AA048343	standard; Protein: 773 AA.
3	AA048343	standard; Protein: 773 AA.
4	AA048343	standard; Protein: 773 AA.
5	AA048343	standard; Protein: 773 AA.
6	AA048343	standard; Protein: 773 AA.
7	AA048343	standard; Protein: 773 AA.
8	AA048343	standard; Protein: 773 AA.
9	AA048343	standard; Protein: 773 AA.
10	AA048343	standard; Protein: 773 AA.
11	AA048343	standard; Protein: 773 AA.
12	AA048343	standard; Protein: 773 AA.
13	AA048343	standard; Protein: 773 AA.
14	AA048343	standard; Protein: 773 AA.
15	AA048343	standard; Protein: 773 AA.
16	AA048343	standard; Protein: 773 AA.
17	AA048343	standard; Protein: 773 AA.
18	AA048343	standard; Protein: 773 AA.
19	AA048343	standard; Protein: 773 AA.
20	AA048343	standard; Protein: 773 AA.
21	AA048343	standard; Protein: 773 AA.
22	AA048343	standard; Protein: 773 AA.
23	AA048343	standard; Protein: 773 AA.
24	AA048343	standard; Protein: 773 AA.
25	AA048343	standard; Protein: 773 AA.
26	AA048343	standard; Protein: 773 AA.
27	AA048343	standard; Protein: 773 AA.
28	AA048343	standard; Protein: 773 AA.
29	AA048343	standard; Protein: 773 AA.
30	AA048343	standard; Protein: 773 AA.
31	AA048343	standard; Protein: 773 AA.
32	AA048343	standard; Protein: 773 AA.
33	AA048343	standard; Protein: 773 AA.
34	AA048343	standard; Protein: 773 AA.
35	AA048343	standard; Protein: 773 AA.
36	AA048343	standard; Protein: 773 AA.
37	AA048343	standard; Protein: 773 AA.
38	AA048343	standard; Protein: 773 AA.
39	AA048343	standard; Protein: 773 AA.
40	AA048343	standard; Protein: 773 AA.
41	AA048343	standard; Protein: 773 AA.
42	AA048343	standard; Protein: 773 AA.
43	AA048343	standard; Protein: 773 AA.
44	AA048343	standard; Protein: 773 AA.
45	AA048343	standard; Protein: 773 AA.

1. S. pneumoniae Sp13 polypeptide.

2. S. pneumoniae Sp13 polypeptide.

3. S. pneumoniae Sp13 polypeptide.

4. S. pneumoniae Sp13 polypeptide.

5. S. pneumoniae Sp13 polypeptide.

6. S. pneumoniae Sp13 polypeptide.

7. S. pneumoniae Sp13 polypeptide.

8. S. pneumoniae Sp13 polypeptide.

9. S. pneumoniae Sp13 polypeptide.

10. S. pneumoniae Sp13 polypeptide.

11. S. pneumoniae Sp13 polypeptide.

12. S. pneumoniae Sp13 polypeptide.

13. S. pneumoniae Sp13 polypeptide.

14. S. pneumoniae Sp13 polypeptide.

15. S. pneumoniae Sp13 polypeptide.

16. S. pneumoniae Sp13 polypeptide.

17. S. pneumoniae Sp13 polypeptide.

18. S. pneumoniae Sp13 polypeptide.

19. S. pneumoniae Sp13 polypeptide.

20. S. pneumoniae Sp13 polypeptide.

21. S. pneumoniae Sp13 polypeptide.

22. S. pneumoniae Sp13 polypeptide.

23. S. pneumoniae Sp13 polypeptide.

24. S. pneumoniae Sp13 polypeptide.

25. S. pneumoniae Sp13 polypeptide.

26. S. pneumoniae Sp13 polypeptide.

27. S. pneumoniae Sp13 polypeptide.

28. S. pneumoniae Sp13 polypeptide.

29. S. pneumoniae Sp13 polypeptide.

30. S. pneumoniae Sp13 polypeptide.

31. S. pneumoniae Sp13 polypeptide.

32. S. pneumoniae Sp13 polypeptide.

33. S. pneumoniae Sp13 polypeptide.

34. S. pneumoniae Sp13 polypeptide.

35. S. pneumoniae Sp13 polypeptide.

36. S. pneumoniae Sp13 polypeptide.

37. S. pneumoniae Sp13 polypeptide.

38. S. pneumoniae Sp13 polypeptide.

39. S. pneumoniae Sp13 polypeptide.

40. S. pneumoniae Sp13 polypeptide.

41. S. pneumoniae Sp13 polypeptide.

42. S. pneumoniae Sp13 polypeptide.

43. S. pneumoniae Sp13 polypeptide.

44. S. pneumoniae Sp13 polypeptide.

45. S. pneumoniae Sp13 polypeptide.

PR 14-MAY-1999 59US-0134221.
 PR 14-MAY-1999 59US-0134370.
 PR 18-MAY-1999 59US-0134768.
 PR 18-MAY-1999 59US-0135121.
 PR 20-MAY-1999 59US-0135124.
 PR 21-MAY-1999 59US-0135353.
 PR 24-MAY-1999 59US-0135659.
 PR 27-MAY-1999 59US-0135821.
 PR 28-MAY-1999 59US-0135822.
 PR 28-MAY-1999 59US-0135782.
 PR 01-JUN-1999 59US-0137222.
 PR 01-JUN-1999 59US-0137223.
 PR 04-JUN-1999 59US-0137502.
 PR 07-JUN-1999 59US-0137502.
 PR 07-JUN-1999 59US-0137724.
 PR 08-JUN-1999 59US-0138094.
 PR 10-JUN-1999 59US-0138287.
 PR 14-JUN-1999 59US-0139119.
 PR 16-JUN-1999 59US-0139462.
 PR 16-JUN-1999 59US-0139463.
 PR 17-JUN-1999 59US-0139462.
 PR 18-JUN-1999 59US-0139454.
 PR 18-JUN-1999 59US-0139455.
 PR 18-JUN-1999 59US-0139458.
 PR 18-JUN-1999 59US-0139459.
 PR 18-JUN-1999 59US-0139461.
 PR 18-JUN-1999 59US-0139462.
 PR 18-JUN-1999 59US-0139723.
 PR 18-JUN-1999 59US-0139723.
 PR 21-JUN-1999 59US-0139817.
 PR 22-JUN-1999 59US-0139899.
 PR 23-JUN-1999 59US-0140054.
 PR 24-JUN-1999 59US-0140055.
 PR 28-JUN-1999 59US-0140823.
 PR 30-JUN-1999 59US-0142827.
 PR 01-JUL-1999 59US-0141842.
 PR 01-JUL-1999 59US-0141842.
 PR 02-JUL-1999 59US-0142803.
 PR 08-JUL-1999 59US-0142803.
 PR 09-JUL-1999 59US-0142920.
 PR 11-JUL-1999 59US-0143542.
 PR 14-JUL-1999 59US-0143544.
 PR 15-JUL-1999 59US-0143644.
 PR 15-JUL-1999 59US-0144005.
 PR 16-JUL-1999 59US-0144006.
 PR 19-JUL-1999 59US-0144235.
 PR 19-JUL-1999 59US-0144331.
 PR 19-JUL-1999 59US-0144331.
 PR 19-JUL-1999 59US-0144331.
 PR 19-JUL-1999 59US-0144334.
 PR 19-JUL-1999 59US-0144335.
 PR 20-JUL-1999 59US-0144622.
 PR 20-JUL-1999 59US-0144684.
 PR 21-JUL-1999 59US-0144684.
 PR 21-JUL-1999 59US-0145088.
 PR 22-JUL-1999 59US-0145085.
 PR 22-JUL-1999 59US-0145087.
 PR 22-JUL-1999 59US-0145132.
 PR 23-JUL-1999 59US-0145145.
 PR 23-JUL-1999 59US-0145238.
 PR 23-JUL-1999 59US-0145238.
 PR 26-JUL-1999 59US-0145236.
 PR 27-JUL-1999 59US-0145913.
 PR 27-JUL-1999 59US-0145918.
 PR 28-JUL-1999 59US-0145919.
 PR 02-AUG-1999 59US-0146286.
 PR 02-AUG-1999 59US-0146286.
 PR 02-AUG-1999 59US-0146288.
 PR 02-AUG-1999 59US-0146359.
 PR 02-AUG-1999 59US-0146359.
 PR 04-AUG-1999 59US-0147204.
 PR 04-AUG-1999 59US-0147204.
 PR 05-AUG-1999 59US-0147302.
 PR 05-AUG-1999 59US-0147302.
 PR 06-AUG-1999 59US-0147303.
 PR 06-AUG-1999 59US-0147466.
 PR 09-AUG-1999 59US-0147466.
 PR 09-AUG-1999 59US-0147466.
 PR 10-AUG-1999 59US-0148171.
 PR 11-AUG-1999 59US-0148171.
 PR 11-AUG-1999 59US-0148171.
 PR 13-AUG-1999 59US-0148684.
 PR 13-AUG-1999 59US-0148684.
 PR 16-AUG-1999 59US-0149368.
 PR 17-AUG-1999 59US-0149368.
 PR 20-AUG-1999 59US-0149723.
 PR 20-AUG-1999 59US-0149723.
 PR 20-AUG-1999 59US-0149729.
 PR 22-AUG-1999 59US-0149930.
 PR 25-AUG-1999 59US-0150566.
 PR 26-AUG-1999 59US-0150884.
 PR 27-AUG-1999 59US-0150884.
 PR 27-AUG-1999 59US-0151067.
 PR 30-AUG-1999 59US-0151303.
 PR 30-AUG-1999 59US-0151303.
 PR 01-SEP-1999 59US-0151930.
 PR 07-SEP-1999 59US-0152363.
 PR 10-SEP-1999 59US-0153070.
 PR 11-SEP-1999 59US-0153070.
 PR 15-SEP-1999 59US-0154018.
 PR 16-SEP-1999 59US-0154039.
 PR 20-SEP-1999 59US-0154779.
 PR 20-SEP-1999 59US-0154779.
 PR 23-SEP-1999 59US-0155486.
 PR 24-SEP-1999 59US-0155659.
 PR 28-SEP-1999 59US-0156488.
 PR 28-SEP-1999 59US-0156488.
 PR 04-OCT-1999 59US-0157117.
 PR 05-OCT-1999 59US-0157753.
 PR 06-OCT-1999 59US-0157855.
 PR 08-OCT-1999 59US-0158232.
 PR 12-OCT-1999 59US-0158369.
 PR 13-OCT-1999 59US-0158233.
 PR 13-OCT-1999 59US-0158235.
 PR 13-OCT-1999 59US-0158285.
 PR 14-OCT-1999 59US-0159239.
 PR 14-OCT-1999 59US-0159330.
 PR 14-OCT-1999 59US-0159330.
 PR 14-OCT-1999 59US-0159638.
 PR 14-OCT-1999 59US-0159637.
 PR 18-OCT-1999 59US-0162544.
 PR 18-OCT-1999 59US-0162544.
 PR 21-OCT-1999 59US-0162767.
 PR 21-OCT-1999 59US-0162767.
 PR 21-OCT-1999 59US-0162768.
 PR 21-OCT-1999 59US-0162770.
 PR 21-OCT-1999 59US-0162770.
 PR 22-OCT-1999 59US-0162815.
 PR 22-OCT-1999 59US-0162815.
 PR 22-OCT-1999 59US-0162815.
 PR 25-OCT-1999 59US-0164044.
 PR 25-OCT-1999 59US-0164044.

PR 14-MAY-1999 9905-0134218.
 PR 14-MAY-1999 9905-0144315.
 PR 14-MAY-1999 9905-0143770.
 PR 14-MAY-1999 9905-0134766.
 PR 18-MAY-1999 9905-0144441.
 PR 18-MAY-1999 9905-0144441.
 PR 21-MAY-1999 9905-0135553.
 PR 24-MAY-1999 9905-0135623.
 PR 24-MAY-1999 9905-0136623.
 PR 24-MAY-1999 9905-0136782.
 PR 01-JUN-1999 9905-0137222.
 PR 01-JUN-1999 9905-0137724.
 PR 07-JUN-1999 9905-0138094.
 PR 10-JUN-1999 9905-0138540.
 PR 14-JUN-1999 9905-0139113.
 PR 16-JUN-1999 9905-0139553.
 PR 16-JUN-1999 9905-0139653.
 PR 18-JUN-1999 9905-0139454.
 PR 18-JUN-1999 9905-0139455.
 PR 18-JUN-1999 9905-0139456.
 PR 18-JUN-1999 9905-0139458.
 PR 18-JUN-1999 9905-0139459.
 PR 18-JUN-1999 9905-0139460.
 PR 18-JUN-1999 9905-0139461.
 PR 18-JUN-1999 9905-0139463.
 PR 18-JUN-1999 9905-0139750.
 PR 18-JUN-1999 9905-0139845.
 PR 22-JUN-1999 9905-0139899.
 PR 22-JUN-1999 9905-0140153.
 PR 23-JUN-1999 9905-0140353.
 PR 23-JUN-1999 9905-0140353.
 PR 28-JUN-1999 9905-0140823.
 PR 29-JUN-1999 9905-0140931.
 PR 29-JUN-1999 9905-0141487.
 PR 01-JUL-1999 9905-0141534.
 PR 02-JUL-1999 9905-0142055.
 PR 06-JUL-1999 9905-0142250.
 PR 06-JUL-1999 9905-0142250.
 PR 09-JUL-1999 9905-0142820.
 PR 12-JUL-1999 9905-0142877.
 PR 13-JUL-1999 9905-0143542.
 PR 13-JUL-1999 9905-0143542.
 PR 15-JUL-1999 9905-0144005.
 PR 16-JUL-1999 9905-0144086.
 PR 16-JUL-1999 9905-0144131.
 PR 16-JUL-1999 9905-0144131.
 PR 19-JUL-1999 9905-0144432.
 PR 19-JUL-1999 9905-0144432.
 PR 20-JUL-1999 9905-0144352.
 PR 20-JUL-1999 9905-0144642.
 PR 21-JUL-1999 9905-0146644.
 PR 21-JUL-1999 9905-0145086.
 PR 21-JUL-1999 9905-0145086.
 PR 22-JUL-1999 9905-0145087.
 PR 22-JUL-1999 9905-0145089.
 PR 23-JUL-1999 9905-0145192.
 PR 23-JUL-1999 9905-0145218.
 PR 23-JUL-1999 9905-0145218.

PR 23-JUL-1999 9905-0145224.
 PR 26-JUL-1999 9905-0145276.
 PR 26-JUL-1999 9905-0145318.
 PR 27-JUL-1999 9905-0145318.
 PR 27-JUL-1999 9905-0145319.
 PR 28-JUL-1999 9905-0145551.
 PR 28-JUL-1999 9905-0145551.
 PR 02-AUG-1999 9905-0146388.
 PR 02-AUG-1999 9905-0146389.
 PR 03-AUG-1999 9905-0147038.
 PR 04-AUG-1999 9905-0147002.
 PR 04-AUG-1999 9905-0147002.
 PR 05-AUG-1999 9905-0147192.
 PR 05-AUG-1999 9905-0147260.
 PR 06-AUG-1999 9905-0147416.
 PR 06-AUG-1999 9905-0147493.
 PR 09-AUG-1999 9905-0147935.
 PR 09-AUG-1999 9905-0147935.
 PR 11-AUG-1999 9905-0148313.
 PR 12-AUG-1999 9905-0148341.
 PR 13-AUG-1999 9905-0148665.
 PR 13-AUG-1999 9905-0149368.
 PR 17-AUG-1999 9905-0149175.
 PR 18-AUG-1999 9905-0149426.
 PR 20-AUG-1999 9905-0149923.
 PR 20-AUG-1999 9905-0149923.
 PR 23-AUG-1999 9905-0149902.
 PR 23-AUG-1999 9905-0150564.
 PR 26-AUG-1999 9905-0150864.
 PR 27-AUG-1999 9905-0151065.
 PR 27-AUG-1999 9905-0151065.
 PR 30-AUG-1999 9905-0151303.
 PR 31-AUG-1999 9905-0151438.
 PR 01-SEP-1999 9905-0152130.
 PR 01-SEP-1999 9905-0152130.
 PR 01-SEP-1999 9905-0152130.
 PR 11-SEP-1999 9905-0153758.
 PR 11-SEP-1999 9905-0154418.
 PR 11-SEP-1999 9905-0154418.
 PR 20-SEP-1999 9905-0154739.
 PR 22-SEP-1999 9905-0155139.
 PR 21-SEP-1999 9905-0155488.
 PR 21-SEP-1999 9905-0156456.
 PR 28-SEP-1999 9905-0156456.
 PR 29-SEP-1999 9905-0156596.
 PR 01-OCT-1999 9905-0157111.
 PR 01-OCT-1999 9905-0157111.
 PR 06-OCT-1999 9905-0157865.
 PR 07-OCT-1999 9905-0158029.
 PR 08-OCT-1999 9905-0158232.
 PR 11-OCT-1999 9905-0158291.
 PR 11-OCT-1999 9905-0158291.
 PR 13-OCT-1999 9905-0159294.
 PR 13-OCT-1999 9905-0159294.
 PR 14-OCT-1999 9905-0159310.
 PR 14-OCT-1999 9905-0159310.
 PR 14-OCT-1999 9905-0159637.
 PR 16-OCT-1999 9905-0159584.
 PR 21-OCT-1999 9905-0160741.
 PR 21-OCT-1999 9905-0160767.
 PR 21-OCT-1999 9905-0160770.
 PR 21-OCT-1999 9905-0160814.
 PR 21-OCT-1999 9905-0160815.
 PR 22-OCT-1999 9905-0160981.

1	XX	antitumor gene therapy; cancer; proliferative disorder; hypertension;
2	XX	neurodegenerative disorder; osteoarthritis; graft vs host disease;
3	XX	cardiovascular disease; diabetes mellitus; hyperproliferative disease;
4	XX	severe combined immunodeficiency; leukemia; autoimmune disorders; asthma;
5	XX	allergy; aplastic anemia; neonatal thrombocytosis; burn; wound;
6	XX	bone damage; cartilage disease; antiinflammatory disease; coagulation;
7	XX	thrombosis; contraceptive.
8	XX	
9	XX	Homio sapiens.
10	XX	NC0200054173.42.
11	XX	05-OCT-2000.
12	XX	
13	XX	31-MAR-2000; 2000MO-0508621.
14	XX	
15	XX	31-MAR-1999; 9905-0127607.
16	XX	02-APR-1999; 9905-0127636.
17	XX	05-APR-1999; 9905-0127728.
18	XX	10-MAR-2000; 100505-0540760.
19	XX	
20	XX	(CUBA) - CUBAGEN CORP.
21	XX	
22	XX	Shimkete BA, leach M;
23	XX	WPI; 2000-6026257.
24	XX	W-PS09; ACT7106.
25	XX	
26	XX	Novel nucleic acids and peptides derived from open reading frame X,
27	XX	useful for treating e.g. cancer, proliferative disorders,
28	XX	neurodegenerative disorders and cardiovascular disease -
29	XX	
30	XX	Claim 11: Page 4497-4498, 5507pp; English.
31	XX	
32	XX	AACT7446 to AACT7606 encodes the protein given in AAB04237 to AAB43397,
33	XX	which represent the human open reading frames 1 to 3161. The ORF
34	XX	antiproliferic; antiproliferant; antiproliferic; neuroprotective; cytotoxic;
35	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
36	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
37	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
38	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
39	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
40	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
41	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
42	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
43	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
44	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
45	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
46	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
47	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
48	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
49	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
50	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
51	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
52	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
53	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
54	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
55	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
56	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
57	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
58	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
59	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
60	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
61	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
62	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
63	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
64	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
65	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
66	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
67	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
68	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
69	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
70	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
71	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
72	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
73	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
74	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
75	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
76	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
77	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
78	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
79	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
80	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
81	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
82	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
83	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
84	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
85	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
86	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
87	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
88	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
89	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
90	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
91	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
92	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
93	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
94	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
95	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
96	XX	antiproliferic; antiproliferant; antiproliferic; immunoprotective;
97	XX</	

	D6	12 KEPPVHXKXIKIYQNMNA-VENKI-KFSPDSWSTFRHPTOTNNIDR_166
	PB	RESULT 37
	ID	ABP7J209 standard; Protein; 635 AA.
	XZ	ABP7J209
	XZ	ABP7J209;
	XZ	30-JUN-2003 {first entry}
	XZ	Candida albicans essential protein SSO ID NO 7046.
	XZ	Fungus; yeast; eukaryotic; promoter; GRIFF strain; biosynthesis; signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal.
	XZ	Candida albicans.
	XZ	M0200253728-A2.
	XZ	11-JUL-2002.
	PD	26-DIC-2001; 2001WO-0859486.
	PF	29-DEC-2001; 2000US-259128P. 20-FEB-2001; 2001US-0792024. 22-AUG-2001; 2001US-314050P.
	PR	(EUF-) ELITRA PHARM INC.
	PX	Romer T., Jiang B., Boone C., Bussey H., Olsen KJ.; WPI; 2002-566694/60. N-PDB; AB231755-
	PX	N-PDB; AB231755-
	P7	Claim 44: SEQ ID NO 7046, 167bp + Sequence listing; English.
	P7	The invention relates to constructing (M) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement of another coding sequence, and/or replacing one allele with a promoter fragment, thereby enabling recombination of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M) is useful for constructing a strain of diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that encodes a drug target, a gene that encodes a component of a fungal agent an antifungal agent that inhibit the growth of a mammalian disease. (M) is useful for identifying a compound which modulates the activity of a gene product, preferably metabolic activity, transcriptional regulation, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and/or essential Candida albicans proteins used in the method of the invention. Note: The sequence data for this patent is not represented in the printed the European Patent Office.
	SU	Sequence 635 AA).
	XX	Blast Search
	XX	Query: Similarity: 10.7% Score: 90.5; DB: Z; length 635;
	XX	BLAST result similarity: 22.2%; E-value: 0.0000000e+000


```

XX Xu X, Yang P, He J, Phan L, He M, Ye Y, Shen Y, Kodira C;
PI NPI; 2001-355877/37.
DR N-P008; A0682788.
XX Primary nucleotide sequence of the shrimp white spot Bacilliform virus
PI (6889), useful for producing viral polypeptides that can be used to
PI screen for agents that are useful for treating MSV infection -
XX Claim 1; Figure 3; 626pp; English.
XX
XX The invention provides the primary nucleotide sequence of the MSV genome
CC (A0682889), predicted transcript sequence (A0682889-A0682893) and
CC (A0682894-A0682900), and the amino acid sequence of the MSV proteins
CC (A0682940-63160) suitable for use as primers or probes. The nucleic acid
CC molecules and proteins of the invention are useful for diagnosis and
CC monitoring viral infection. In addition, the invention provides a method
CC for screening for agents that are useful for treating MSV infection.
CC The nucleic acid molecules are also useful as antisense constructs to
CC control viral gene expression in infected cells and tissues and to create
CC transgenic viral resistant shrimp.
XX
XX Sequence 1141 AA;
50
Query Match 18 44; Score 88.5; DB 22; Length 1141;
Similarity 23 41; Positives 25;
Matches 30; Conservative 31; Mismatches 43; Indels 25; Gaps 4;
OY 35 STTWERDPLVYKGLREKVGPGHRTSGRQ--NDQATYTNLSQRTFVYKRTK 92
DB 621 SVRRERE-----RRQVEEREHVRRHSDNDQDA-----PQEDNE 662
OY 93 KKKRNRKQPTFDVSKKGNQVNSGLNSNRKNDQRRHSQSGSTGDTATYTDNN 152
DB 663 KKKRNRKQ-----QQPRHSNKNHRRQKQKQPPRRHNDALSDSDSSSSSS 117
OY 153 TGGKSTNN 161
DB 718 SSSSSSSSS 726

```

Search completed: February 10, 2004, 10:53:56
 Job time : 38.4525 secs